

## SEQUENCE LISTING

<110> Ledbetter, Jeffrey

Hayden-Ledbetter, Martha

<120> Binding Domain-Immunoglobulin Fusion Proteins

<130> 390069.401

<140> US

<141> 2002-01-17

<150> US 09/765,208

<151> 2001-01-17

<160> 38

<170> PatentIn version 3.0

<210> 1

<211> 812

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>

<221> sig\_peptide

<222> (13)..(78)

<220>

<221> V\_region

<222> (79)..(396)

<223> light chain variable region for anti-CD20 scFv

<220>

<221> misc\_feature

<222> (397)..(444)

<223> asp-gly3ser(gly4ser)2-ser peptide linker

<220>

<221> V\_region

<222> (445)..(808)

<223> heavy chain variable region for anti-CD20 scFv

<400> 1

```

aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgcta at cagtgcctca      60
gtcataattg ccagaggaca aattgttctc tcccagtctc cagcaatcct gtctgcatct      120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg      180
taccagcaga agccaggatc ctcccccaaa ccttggattt atgccccatc caacctggct      240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc      300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca      360
cccacgttcg gtgctgggac caagctggag ctgaaagggtg gcggtggctc gggcgggtgt      420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg      480
aggcctgggg cctcagtga aatgtcctgc aaggcttctg gctacacatt taccagttac      540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat      600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta      660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg      720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg      780

```

ggcacagggga ccacgggtcac cgtctctgat ca

812

<210> 2

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE HUMAN CHIMERIC FUSION GENE

<220>

<221> misc\_feature

<222> (13)..(807)

<223> MURINE ANTI-HUMAN CD20 scFv

<220>

<221> C\_region

<222> (808)..(1513)

<223> HUMAN IgG1 Fc TAIL, WILD TYPE HINGE, CH2 AND CH3

<400> 2

aagcttgccg ccatggattt tcaagtgcag attttcagct tcttgctaata cagtgttca	60
gtcataattg ccagaggaca aattgttctc tcccagtctc cagcaatcct gtctgcatct	120
ccagggggaga aggtcaccaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg	180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctgget	240
tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcacaatc	300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca	360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt	420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg	480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac	540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat	600

```

ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctcagcagcc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttgtga caaaactcac 840
acatgcccac cgtgcccagc acctgaactc ctgggggggac cgtcagtctt cctcttcccc 900
ccaaaacca aggacacct catgatctcc cggaccctg aggtcacatg cgtggtggtg 960
gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020
cataatgcc aagacaaagg gggggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080
gtcctcaccg tctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140
aacaagccc tcccagcccc catcgagaaa acaatctcca aagccaaagg gcagccccga 1200
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260
ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320
gggcagcgg agaacaacta caagaccag cctcccgtagc tggactccga cggctccttc 1380
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1440
tgctcogtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500
ccgggtaaat gatctaga 1518

```

<210> 3

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE-HUMAN CHIMERIC FUSION GENE

<220>

<221> misc\_feature

<222> (13)..(807)<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> C\_region

<222> (808)..(1513)

<223> HINGE CYSTEINES (826-829; 844-847; 853-856) MUTATED TO SERINES  
PROLINE TO SERINE MUTATION (880-883) IN CH2 DISRUPTS EFFECTOR FUNCTION

<400> 3  
aagcttgccg ccatggattt tcaagtgcag attttcagct tcttgctaatt cagtgtctca 60  
gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct 120  
ccaggggaga aggtcacaaat gacttgacag gccagctcaa gtgtaagtta catgcactgg 180  
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctgggt 240  
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360  
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtgggtc gggcggtgggt 420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
aggcctgggg cctcagtga aatgtcctgc aaggcttctg gctacacatt taccagttac 540  
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
gtctattttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttctga caaaactcac 840  
acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 900  
ccaaaaccca aggacacct catgatctcc cggacccttg aggtcacatg cgtgggtgggtg 960  
gacgtgagcc acgaagacct tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 1020  
cataatgcc aagacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080  
gtctcaccg tctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 1140  
aacaagccc tcccagcccc catcgagaaa acaatctcca aagccaaagg gcagccccga 1200  
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260  
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320  
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1380

ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtctttctca 1440  
 tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500  
 ccgggtaaat gatctaga 1518

<210> 4

<211> 1518

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE-HUMAN CHIMERIC FUSION GENE

<220>

<221> misc\_feature

<222> (13)..(807)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> C\_region

<222> (808)..(1513)

<223> HINGE CYSTEINES MUTATED TO SERINES (826-829; 844-847; 853-856)  
 WILD TYPE CH2 AND CH3 DOMAINS MEDIATE EFFECTOR FUNCTIONS

<400> 4

aagcttgccg ccatggattt tcaagtgcag attttcagct tcttgctaatt cagtgcctca 60  
 gtcataattg ccagaggaca aattgtttctc tcccagtctc cagcaatcct gtctgcatct 120  
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180  
 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
 tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
 agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360  
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgt 420

ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctggtg 480  
 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
 ggcacaggga ccacggtcac cgtctctgat caggagccca aatcttctga caaaactcac 840  
 acatccccac cgtccccagc acctgaactc ctggggggac cgtcagtctt cctcttcccc 900  
 ccaaaacca aggacacct catgatctcc cggaccctg aggtcacatg cgtgggtggtg 960  
 gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggagggtg 1020  
 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 1080  
 gtctcaccg tctgcacca ggactggctg aatggcaagg agtacaagt caaggtctcc 1140  
 aacaaagccc tccagcccc catcgagaaa acaatctcca aagccaaagg gcagccccga 1200  
 gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260  
 ctgacctgcc tggtaaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 1320  
 gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1380  
 ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1440  
 tgctccgtga tgcattaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1500  
 ccgggtaaat gatctaga 1518

<210> 5

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE HUMAN CHIMERIC FUSION GENE

<220>

<221> misc\_feature

<222> (1)..(796)

<223> MOUSE ANTI HUMAN CD20 SCFV

<220>

<221> N\_region

<222> (797)..(864)

<223> HUMAN IGA HINGE REGION

<220>

<221> C\_region

<222> (865)..(1518)

<223> HUMAN IGG1 CH2 AND CH3 WILD TYPE FC DOMAIN

<400> 5  
atggattttc aagtgcagat tttcagcttc ctgctaataca gtgcttcagt cataattgcc 60  
agaggacaaa ttgttctctc ccagtctcca gcaatcctgt ctgcatctcc aggggagaag 120  
gtcacaatga cttgcagggc cagctcaagt gtaagttaca tgcaactgga ccagcagaag 180  
ccaggatcct cccccaacc ctggatttat gcccaccca acctggcttc tggagtcctt 240  
gctcgcttca gtggcagtggt gtctgggacc tcttactctc tcacaatcag cagagtggag 300  
gctgaagatg ctgccactta ttactgccag cagtggagtt ttaaccacc cacgttcggt 360  
gctgggacca agctggagct gaaagatggc ggtggctcgg gcggtggtgg atctggagga 420  
ggtgggagct ctcaggctta tctacagcag tctggggctg agctggtgag gcctggggcc 480  
tcagtgaaga tgtcctgcaa ggcttctggc tacacattta ccagttacaa tatgcactgg 540  
gtaaagcaga cacctagaca gggcctggaa tggattggag ctatttatcc aggaaatggt 600  
gatacttcct acaatcagaa gttcaagggc aaggccacac tgactgtaga caaatcctcc 660  
agcacagcct acatgcagct cagcagcctg acatctgaag actctgcggt ctatttctgt 720  
gcaagagtgg tgtactatag taactcttac tgggtacttcg atgtctgggg cacagggacc 780  
acggtcacccg tctctgatca gccagttccc tcaactccac ctaccccatc tccctcaact 840  
ccacctacc cactctcctc atgcgcacct gaactcctgg ggggaccgtc agtcttctc 900



```

ttccccccaa aaccceaagga caccctcatg atctcccga cccctgaggt cacatgctg 960
gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1020
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 1080
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1140
gtctccaaca aagccctccc agcccccatc gagaaaacaa tctccaaagc caaagggcag 1200
ccccgagaac cacaggtgta caccctgccc ccatcccggg atgagctgac caagaaccag 1260
gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1320
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1380
tccttcttcc tctacagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1440
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1500
ctgtctccgg gtaaattgatc taga 1524

```

<210> 6

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC HUMAN PARTIAL FUSION GENE

<220>

<221> misc\_feature

<222> (1)..(705)

<223> HINGE CYSTEINES MUTATED TO SERINES (19-21; 37-39; 46-48)

<400> 6

```

gatcaggagc ccaaattcttc tgacaaaact cacacatccc caccgtcccc agcacctgaa 60
ctcctggggg gaccgtcagt cttcctcttc cccccaaac ccaaggacac cctcatgac 120
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 180
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 240
gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 300

```

```

ctgaatggca aggagtacaa gtgcaaggtc tccaacaaag ccctcccagc ccccatcgag 360
aaaacaatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 420
tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat 480
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 540
acgcctcccg tgctggactc cgacggctcc ttcttctctt acagcaagct caccgtggac 600
aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 660
aaccactaca cgcagaagag cctctccctg tctccgggta aatgatctag a 711

```

```
<210> 7
```

```
<211> 729
```

```
<212> DNA
```

```
<213> Artificial Sequence
```

```
<220>
```

```
<223> SYNTHETIC HUMAN PARTIAL FUSION GENE
```

```
<220>
```

```
<221> N_region
```

```
<222> (1)..(69)
```

```
<223> HUMAN IGA HINGE
```

```
<220>
```

```
<221> C_region
```

```
<222> (70)..(723)
```

```
<223> HUMAN WILD TYPE IGG1 CH2 AND CH3, FC
```

```
<400> 7
```

```

gatcagccag ttccctcaac tccacctacc ccctctccct caactccacc taccccatct 60
ccctcatgcg cacctgaact cctgggggga ccgtcagtct tcctcttccc cccaaaaccc 120
aaggacaccc tcatgatctc ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc 180
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 240

```

```

aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtgggtcag cgtcctcacc 300
gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 360
ctcccagccc ccatcgagaa aacaatctcc aaagccaaag ggcagccccg agaaccacag 420
gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accagggtcag cctgacctgc 480
ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 540
gagaacaact acaagaccac gcctcccggtg ctggactccg acggctcctt cttcctctac 600
agcaagctca ccgtggacaa gagcagggtg cagcagggga acgtcttctc atgctccgtg 660
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa 720
tgatctaga 729

```

<210> 8

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>

<221> misc\_feature

<222> (13)..(72)

<223> LIGHT CHAIN LEADER PEPTIDE

<220>

<221> V\_region

<222> (73)..(405)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<220>

<221> misc\_feature

<222> (406)..(450)

<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

<220>

<221> V\_region

<222> (454)..(825)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<400> 8  
aagcttgccg ccatggagac agacacactc ctgctatggg tgctgctgct ctgggttcca 60  
ggctccactg gtgacattgt gctgacccaa tctccagctt ctttggtgt gtctctaggg 120  
cagagggcca ccatctcctg caaggccagc caaagtgtg attatgatgg tgatagttat 180  
ttgaactggt accaacagat tccaggacag ccacccaaac tcctcatcta tgatgcatcc 240  
aatctagttt ctgggatccc acccaggttt agtggcagtg ggtctgggac agacttcacc 300  
ctcaacatcc atcctgtgga gaaggtggat gctgcaacct atcactgtca gcaaagtact 360  
gaggatccgt ggacgttcgg tggaggcacc aagctggaaa tcaaagggtg cgggtggctcg 420  
ggcgggtggtg ggtcgggtgg cggcggatcg tcacaggttc agctgcagca gtctggggct 480  
gagctggtga ggctgggtc ctcagtgaag atttcctgca aggcttctgg ctatgcattc 540  
agtagctact ggatgaactg ggtgaagcag aggcctggac agggctctga gtggattgga 600  
cagatttggc ctggagatgg tgatactaac tacaatggaa agttcaaggg taaagccact 660  
ctgactgcag acgaatcctc cagcacagcc tacatgcaac tcagcagcct agcatctgag 720  
gactctgcgg tctatttctg tgcaagacgg gagactacga cggtaggccg ttattactat 780  
gctatggact actgggggtca aggaacctca gtcaccgtct cctca 825

<210> 9

<211> 795

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>

<221> misc\_feature

<222> (13)..(72)

<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

<220>

<221> V\_region

<222> (73)..(393)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<220>

<221> misc\_feature

<222> (394)..(441)

<223> SYNTHETIC LINKER PEPTIDE ENCODED (GLY4SER)3

<220>

<221> V\_region

<222> (442)..(795)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<400> 9  
aagcttgccg ccatggtatc cacagctcag ttccttgggt tgctgctgct gtggcttaca 60  
ggtggcagat gtgacatcca gatgactcag tctccagcct ccctatctgc atctgtggga 120  
gagactgtca ccatcacatg tcgaacaagt gaaaatgttt acagttattt ggcttggtat 180  
cagcagaaac agggaaaatc tcctcagctc ctggtctctt ttgcaaaaac cttagcagaa 240  
ggtgtgccat caaggttcag tggcagtggga tcaggcacac agttttctct gaagatcagc 300  
agcctgcagc ctgaagattc tggaagttat ttctgtcaac atcattccga taatccgtgg 360  
acgttcggtg gaggcaccga actggagatc aaaggtggcg gtggctcggg cggtgggtggg 420  
tcgggtggcg gcggatcgtc agcgggtccag ctgcagcagt ctggacctga gctggaaaag 480

```

cctggcgctt cagtgaagat ttcttgcaag gcttctgggtt actcattcac tggctacaat    540
atgaactggg tgaagcagaa taatggaaag agccttgagt ggattggaaa tattgatcct    600
tattatggtg gtactaccta caaccggaag ttcaagggaaggaggccacatt gactgtagac    660
aaatcctcca gcacagccta catgcagctc aagagtctga catctgagga ctctgcagtc    720
tattactgtg caagatcggg cggccctatg gactactggg gtcaaggaac ctcagtcacc    780
gtctcttctg atcag                                                    795

```

<210> 10

<211> 824

<212> DNA

<213> Artificial Sequence

<220>

<223> SYNTHETIC MOUSE FUSION GENE

<220>

<221> sig\_peptide

<222> (1)..(61)

<223> native light chain leader peptide

<220>

<221> V\_region

<222> (62)..(397)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>

<221> misc\_feature

<222> (398)..(445)

<223> (gly4ser)3 linker peptide

<220>

<221> V\_region

<222> (445)..(818)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>

<221> misc\_feature

<222> (819)..(824)

<223> BclI restriction site

<400> 10

atggagtcac attcccaggt ctttctctcc ctgctgctct gggatatctgg tacctgtggg	60
aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggctact	120
atgaactgta agtccagtc aagtgttttc tacagttcaa atcagaggaa ttatttggcc	180
tggtatcagc agaaaccagg gcagtctccc aaattgctga tctactgggc atctactagg	240
gaatctggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactettacc	300
atcagcagtg tacatactga agacctggca gtttattact gtcatacaatt cctctcttcg	360
tggacgttcg gtggaggcac caagctggaa atcaaaggcg gtggtgggtc ggggtgggtg	420
ggttcgggtg gcggcggatc ttctcaggtc caactgcagc agcctggggc tgaactggtg	480
aagcctggga cttcagtga gctgtcctgc aaggcctctg gctacacctt caccaactac	540
tggatggtct ggggtgaagca gacgcctgga gaaggccttg agtggattgg agaaattatt	600
cctagcaacg gtcgtactaa atacaatgag aagttcaaga gcaaggccac actgactgca	660
gacaaatcct cccgcacagc ctacatgcaa ctacagagcc tggcatctga ggactctgcg	720
gtctattatt gtgcaagaga gatgtccatt attactacgg tactgactcc cggtttgctt	780
actggggcca agggactctg gtcactgtct ctgcagcctg atca	824

<210> 11

<211> 266

<212> PRT

<213> Mus musculus

<220>

<221> INIT\_MET

<222> (1)..(1)

<220>

<221> SIGNAL

<222> (1)..(22)

<220>

<221> DOMAIN

<222> (23)..(128)

<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<220>

<221> SITE

<222> (129)..(144)

<223> ASP-(GLY3SER)-(GLY4SER)2-SER LINKER PEPTIDE

<220>

<221> DOMAIN

<222> (145)..(266)

<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20

<400> 11

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	

Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20				25						30		

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			

Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



50                      55                      60  
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65                      70                      75                      80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
                     85                      90                      95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
                     100                      105                      110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
                     115                      120                      125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
                     130                      135                      140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145                      150                      155                      160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
                     165                      170                      175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
                     180                      185                      190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
                     195                      200                      205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
                     210                      215                      220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225                      230                      235                      240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
                     245                      250                      255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp  
                     260                      265

<210> 12

<211> 271

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(271)

<223> MOUSE ANTI-HUMAN CD19 SCFV

&lt;400&gt; 12

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 1 5 10 15  
 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala  
 20 25 30  
 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser  
 35 40 45  
 Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro  
 50 55 60  
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser  
 65 70 75 80  
 Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 85 90 95  
 Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys  
 100 105 110  
 Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu  
 115 120 125  
 Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 130 135 140  
 Gly Ser Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg  
 145 150 155 160  
 Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe  
 165 170 175  
 Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
 180 185 190  
 Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn  
 195 200 205  
 Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser  
 210 215 220  
 Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val  
 225 230 235 240  
 Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr  
 245 250 255  
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
 260 265 270

&lt;210&gt; 13

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(259)

&lt;223&gt; MOUSE ANTI-HUMAN CD37 SCFV

&lt;400&gt; 13

Met	Val	Ser	Thr	Ala	Gln	Phe	Leu	Gly	Leu	Leu	Leu	Leu	Trp	Leu	Thr
1				5					10					15	

Gly	Gly	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ser
			20					25					30		

Ala	Ser	Val	Gly	Glu	Thr	Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser	Glu	Asn
		35					40					45			

Val	Tyr	Ser	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro
	50					55					60				

Gln	Leu	Leu	Val	Ser	Phe	Ala	Lys	Thr	Leu	Ala	Glu	Gly	Val	Pro	Ser
65					70					75					80

Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ser	Leu	Lys	Ile	Ser
			85						90					95	

Ser	Leu	Gln	Pro	Glu	Asp	Ser	Gly	Ser	Tyr	Phe	Cys	Gln	His	His	Ser
			100					105					110		

Asp	Asn	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Glu	Leu	Glu	Ile	Lys	Gly
		115					120					125			

Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Ala
		130				135						140			

Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Glu	Lys	Pro	Gly	Ala	Ser
145					150					155					160

Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Thr	Gly	Tyr	Asn
				165					170					175	

Met	Asn	Trp	Val	Lys	Gln	Asn	Asn	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly
			180					185					190		

Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys  
195 200 205

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met  
210 215 220

Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala  
225 230 235 240

Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr  
245 250 255

Val Ser Ser

<210> 14

<211> 272

<212> PRT

<213> Mus musculus

<220>

<221> SITE

<222> (1)..(272)

<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser  
1 5 10 15

Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala  
20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Asn Cys Lys Ser Ser Gln Ser  
35 40 45

Val Phe Tyr Ser Ser Asn Gln Arg Asn Tyr Leu Ala Trp Tyr Gln Gln  
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp  
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val His Thr Glu Asp Leu Ala Val Tyr  
100 105 110

Tyr Cys His Gln Phe Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys  
           115                          120                          125  
 Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
       130                          135                          140  
 Gly Gly Ser Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val  
   145                          150                          155                          160  
 Lys Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr  
                           165                          170                          175  
 Phe Thr Asn Tyr Trp Met Val Trp Val Lys Gln Thr Pro Gly Glu Gly  
                           180                          185                          190  
 Leu Glu Trp Ile Gly Glu Ile Ile Pro Ser Asn Gly Arg Thr Lys Tyr  
                           195                          200                          205  
 Asn Glu Lys Phe Lys Ser Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser  
       210                          215                          220  
 Arg Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala  
   225                          230                          235                          240  
 Val Tyr Tyr Cys Ala Arg Glu Met Ser Ile Ile Thr Thr Val Leu Thr  
                           245                          250                          255  
 Pro Gly Leu Leu Thr Gly Ala Lys Gly Leu Trp Ser Leu Ser Leu Gln  
                           260                          265                          270

<210> 15

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125

Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
130 135 140

Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175

Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
210 215 220

Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
225					230					235					240

Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255

Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys

260					265					270					
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly
		275					280					285			
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
	290					295					300				
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
305					310					315					320
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
				325					330					335	
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
			340					345					350		
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
			355				360					365			
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile
	370					375					380				
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
385					390					395					400
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser
			405					410						415	
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
			420				425						430		
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
		435					440					445			
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
	450					455					460				
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
465					470					475					480
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
			485					490						495	
Pro Gly Lys															

&lt;210&gt; 16

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; MOUSE-HUMAN HYBRID FUSION PROTEIN

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(265)

&lt;223&gt; 2H7 SCFV TARGETED TO HUMAN CD20

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (265)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)  
PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

&lt;400&gt; 16

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	
Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		
Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			
Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
		50				55					60				
Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65					70					75					80
Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85					90					95	
Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		
Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			
Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135				140					
Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145					150					155					160



Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser  
 260 265 270  
 Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly  
 275 280 285  
 Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 290 295 300  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 305 310 315 320  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 325 330 335  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 340 345 350  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 355 360 365  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 370 375 380  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 385 390 395 400  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 405 410 415  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 420 425 430  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 435 440 445  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 485 490 495

Pro Gly Lys

<210> 17

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)  
 CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
 50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
 65 70 75 80  
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
 85 90 95  
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
 100 105 110  
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser  
 260 265 270  
 Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly  
 275 280 285  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 290 295 300  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 305 310 315 320  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 325 330 335  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 340 345 350  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
370 375 380

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
420 425 430

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
435 440 445

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
465 470 475 480

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
485 490 495

Pro Gly Lys

<210> 18

<211> 505

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(288)

<223> WILD TYPE IGA HINGE

CD20-HUMAN FUSION PROTEIN

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (289)..(505)

&lt;223&gt; HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

&lt;400&gt; 18

```

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1          5          10          15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20          25          30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35          40          45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50          55          60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65          70          75          80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85          90          95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100         105         110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115         120         125
Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130         135         140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145         150         155         160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165         170         175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180         185         190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195         200         205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210         215         220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

```

225		230		235		240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp						
		245		250		255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr						
		260		265		270
Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys						
		275		280		285
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys						
		290		295		300
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val						
		305		310		315
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr						
		325		330		335
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu						
		340		345		350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His						
		355		360		365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys						
		370		375		380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln						
		385		390		395
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu						
		405		410		415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro						
		420		425		430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn						
		435		440		445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu						
		450		455		460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val						
		465		470		475
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln						
		485		490		495
Lys Ser Leu Ser Leu Ser Pro Gly Lys						
		500		505		

&lt;210&gt; 19

&lt;211&gt; 234

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(234)

<223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)  
WILD TYPE CH2 AND CH3 DOMAINS  
ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp	Gln	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	1	5	10	15
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	20	25	30	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	35	40	45	
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	50	55	60	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	65	70	75	80
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	85	90	95	
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	100	105	110	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	115	120	125	
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	130	135	140	
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	145	150	155	160
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	165	170	175	
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	180	185	190	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	195	200	205	

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
 210 215 220

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 225 230

<210> 20

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (1)..(23)

<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>

<221> DOMAIN

<222> (24)..(240)

<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro  
 1 5 10 15

Pro Thr Pro Ser Pro Ser Cys Ala Pro Glu Leu Leu Gly Gly Pro Ser  
 20 25 30

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
 35 40 45

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro  
 50 55 60

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
 65 70 75 80

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
 85 90 95

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
 100 105 110

SCFVIG FUSION PROTEINS



Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
 115 120 125

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 130 135 140

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
 145 150 155 160

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 165 170 175

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 180 185 190

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 195 200 205

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
 210 215 220

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 225 230 235 240

<210> 21

<211> 1470

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc\_feature

<222> (1)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc\_feature

<222> (814)..(1455)

<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21  
 aagcttgccg ccatggattt tcaagtgcag attttcagct tcoctgctaata cagtgcattca 60  
 gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct 120  
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcaactgg 180  
 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240  
 tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300  
 agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360  
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgggtgg 420  
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480  
 aggctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540  
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600  
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660  
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720  
 gtctattttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780  
 ggcacagggg ccacggtcac cgtctctgat ccaagaagg tggacaagat agaagatgaa 840  
 aggaatcttc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa 900  
 agatccttat ccttactgaa ctgtgaggag attaaaagcc agtttgaagg ctttgtgaag 960  
 gatataatgt taaacaaaga ggagacgaag aaagaaaaca gctttgaaat gcaaaaagg 1020  
 gatcagaatc ctcaaattgc ggcacatgac ataagtgagg ccagcagtaa aacaacatct 1080  
 gtgttacagt gggctgaaaa aggatactac accatgagca acaacttgg aacctggaa 1140  
 aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcacc 1200  
 ttctgttcca atcggaagc ttcgagtcaa gctccattta tagccagcct ctgcctaaag 1260  
 tccccggta gattcgagag aatcttactc agagctgcaa ataccacag ttccgcaaaa 1320  
 ccttgcgggc aacaatccat tcaactggga ggagtatttg aattgcaacc aggtgcttcg 1380  
 gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cacgtccttt 1440  
 ggcttactca aactcgagtg ataacttaga 1470

<210> 22

<211> 1290

<212> DNA

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID

<220>

<221> misc\_feature

<222> (13)..(808)

<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>

<221> misc\_feature

<222> (814)..(1275)

<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22

```

aagcttgccg ccattggattt tcaagtgcag attttcagct tcctgctaata cagtgcattca      60
gtcataattg ccagaggaca aattgtttct tccagctctc cagcaatcct gtctgcatct      120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg      180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct      240
tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc      300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaaccca      360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg      420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt      480
aggcctgggg cctcagtgaat gatgtcctgc aaggcttctg gctacacatt taccagttac      540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat      600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta      660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg      720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg      780

```

```
<210> 23
<211> 43
<212> DNA
<213> Artificial Sequence
<220>
<223> OLIGONUCLEOTIDE
```

```
<210> 24
<211> 74
<212> DNA
<213> Artificial Sequence
<220>
<223> OLIGONUCLEOTIDE
```

<400> 24  
gtcgtcgagc tccacacctcc tccagatcca ccaccgcccg agccaccgcc acctttcagc 60

tccagcttgg tccc

74

<210> 25

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 25

gctgctgagc tctcaggctt atctacagca agtctgg

37

<210> 26

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 26

gttgtctgat cagagacggt gaccgtggtc cc

32

<210> 27

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 27

34

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; OLIGONUCLEOTIDE

44

<210> 29

<211> 35

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> OLIGONUCLEOTIDE

35

<210> 30

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; OLIGONUCLEOTIDE

<400> 30

	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

gtctatataa gcagagctct ggc

23

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 31

cgaggctgat cagcgagctc tagca

25

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> OLIGONUCLEOTIDE

<400> 32

ccgcaatttg aggattctga tcacc

25

<210> 33

<211> 482

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

&lt;220&gt;

&lt;221&gt; SITE

&lt;222&gt; (1)..(266)

&lt;223&gt; MOUSE ANTI-HUMAN CD20 SCFV

&lt;220&gt;

&lt;221&gt; DOMAIN

&lt;222&gt; (268)..(481)

&lt;223&gt; EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

&lt;400&gt; 33

Met	Asp	Phe	Gln	Val	Gln	Ile	Phe	Ser	Phe	Leu	Leu	Ile	Ser	Ala	Ser
1				5					10					15	

Val	Ile	Ile	Ala	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile
			20					25					30		

Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser
		35					40					45			

Ser	Ser	Val	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser
	50					55					60				

Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Pro	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
65				70						75					80

Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile
				85					90					95	

Ser	Arg	Val	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp
			100					105					110		

Ser	Phe	Asn	Pro	Pro	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
		115					120					125			

Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser
	130					135					140				

Gln	Ala	Tyr	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Ala
145					150					155					160

Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr
			165						170					175	

Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Arg	Gln	Gly	Leu	Glu	Trp	Ile
			180					185					190		

Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn	Gln	Lys	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



195                      200                      205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
     210                      215                      220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
     225                      230                      235                      240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
                     245                      250                      255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys  
                     260                      265                      270  
 Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr  
                     275                      280                      285  
 Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys  
                     290                      295                      300  
 Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu  
     305                      310                      315                      320  
 Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly  
                     325                      330                      335  
 Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser  
                     340                      345                      350  
 Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met  
                     355                      360                      365  
 Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys  
     370                      375                      380  
 Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn  
     385                      390                      395                      400  
 Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys  
                     405                      410                      415  
 Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His  
                     420                      425                      430  
 Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val  
                     435                      440                      445  
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro  
     450                      455                      460  
 Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys  
     465                      470                      475                      480  
 Leu Glu

195 200 205  
 210 215 220  
 225 230 235 240  
 245 250 255  
 260 265 270  
 275 280 285  
 290 295 300  
 305 310 315 320  
 325 330 335  
 340 345 350  
 355 360 365  
 370 375 380  
 385 390 395 400  
 405 410 415  
 420 425 430  
 435 440 445  
 450 455 460  
 465 470 475 480

<210> 34

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(266)

<223> MOUSE ANTI-HUMAN SCFV

<220>

<221>

DOMAIN

<222> (268)..(421)

<223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15

Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
20 25 30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60

Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110

20250909 09:50:00

Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
 115 120 125  
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu  
 260 265 270  
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser  
 275 280 285  
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly  
 290 295 300  
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln  
 305 310 315 320  
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr  
 325 330 335  
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser  
 340 345 350  
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala  
 355 360 365  
 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His  
 370 375 380  
 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn  
 385 390 395 400  
 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe  
 405 410 415

Gly Leu Leu Lys Leu Glu  
420

<210> 35

<211> 63

<212> DNA

<213> Homo sapiens

<220>

<221> N\_region

<222> (1)..(63)

<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

<400> 35  
ccagtttcct caactccacc taccatct ccctcaactc cacctacccc atctccctca 60  
tgc 63

<210> 36

<211> 21

<212> PRT

<213> Homo sapiens

<400> 36

Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr  
1 5 10 15

Pro Ser Pro Ser Cys  
20

<210> 37

<211> 763

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6)

&lt;223&gt; BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

&lt;220&gt;

&lt;221&gt; N\_region

&lt;222&gt; (8)..(752)

<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS  
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

<400> 37  
 tgatcagcca gttccctcaa ctccacctac cccatctccc tcaactccac ctaccccatc 60  
 tccctcatgc tgccaccccc gactgtcact gcaccgaccg gccctcgagg acctgtcttt 120  
 aggttcagaa gcgatacctca cgtgcacact gaccggcctg agagatgcct caggtgtcac 180  
 cttcacctgg acgccctcaa gtgggaagag cgctgttcaa ggaccacctg accgtgacct 240  
 ctgtggctgc tacagcgtgt ccagtgtcct gccgggctgt gccgagccat ggaaccatgg 300  
 gaagaccttc acttgactg ctgcctaccc cgagtccaag accccgctaa ccgccaccct 360  
 ctcaaaatcc ggaaacacat tccggcccga ggtccacctg ctgccgccgc cgtcggagga 420  
 gctggccctg aacgagctgg tgacgctgac gtgcctggca cgtggcttca gccccaagga 480  
 tgtgctgggt cgctggctgc aggggtcaca ggagctgccc cgcgagaagt acctgacttg 540  
 ggcaccccg caggagccca gccagggcac caccaccttc gctgtgacca gcatactgcg 600  
 cgtggcagcc gaggactgga agaaggggga caccttctcc tgcattggtg gccacgaggc 660  
 cctgccgctg gccttcacac agaagacctg cgaccgcttg gcgggtaaac ccacccatgt 720  
 caatgtgtct gttgtcatgg cggaggtgga ctgataatct aga 763

&lt;210&gt; 38

&lt;211&gt; 250

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

```
<221>  DOMAIN
<222>  (3) .. (250)
```

<400> 38

Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu His Arg  
20 25 30

Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Ile Leu Thr Cys  
35 40 45

Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr Trp Thr  
50 55 60

Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg Asp Leu  
65 70 75 80

Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Glu Pro  
85 90 95

Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro Glu Ser  
100 105 110

Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr Phe Arg  
115 120 125

Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn  
130 135 140

Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp  
145 150 155 160

Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys  
165 170 175

Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr  
180 185 190

Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys  
195 200 205

Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala  
210 215 220

Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Val  
225 230 235 240

Asn Val Ser Val Val Met Ala Glu Val Asp  
245 250

[illegible]